1.59

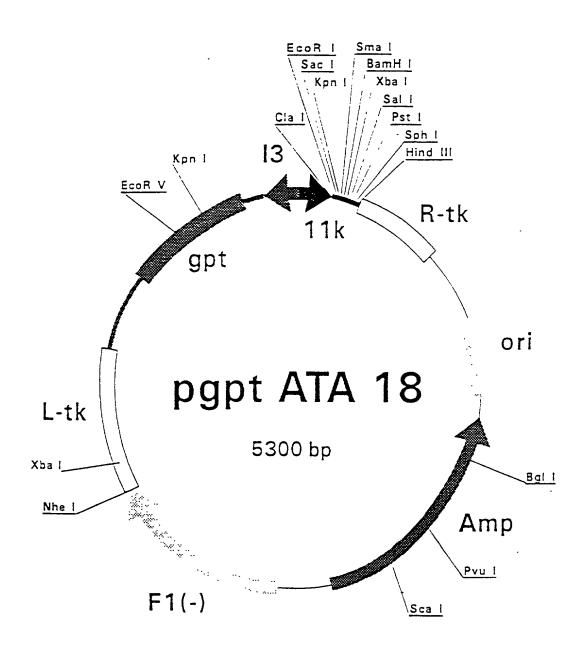


FIGURE 1

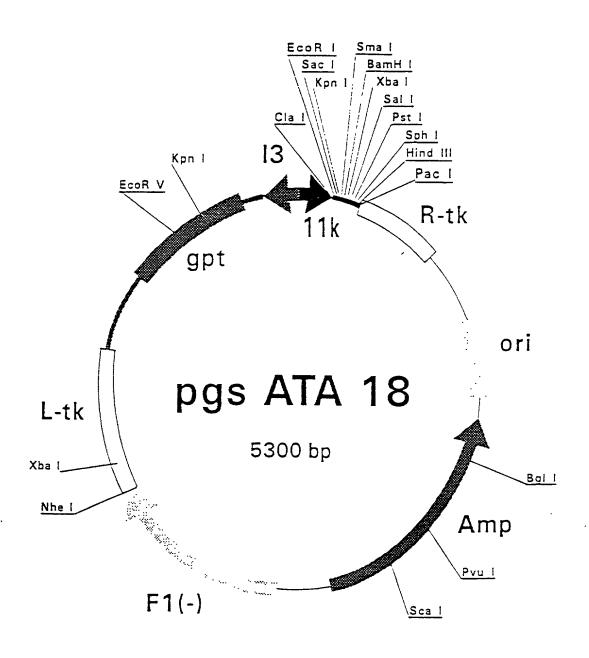


FIGURE 2

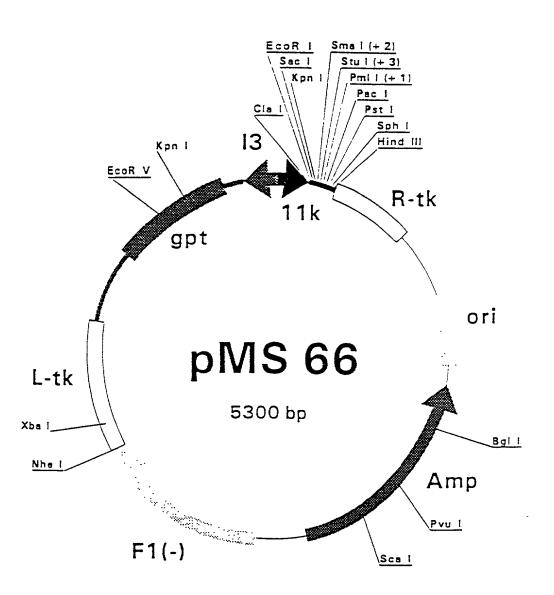


FIGURE 3

4 / 5 9

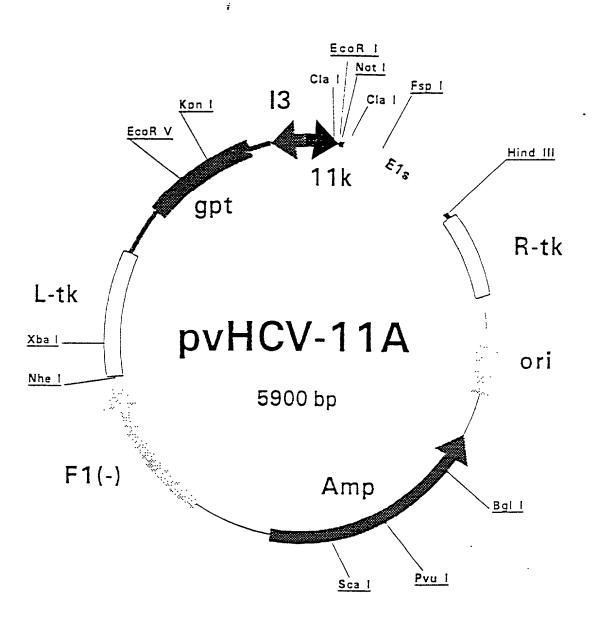
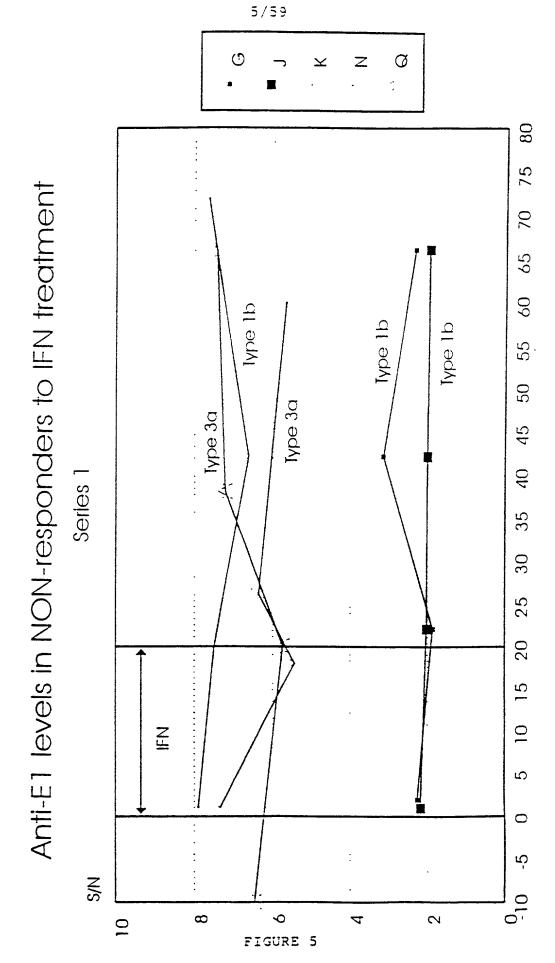


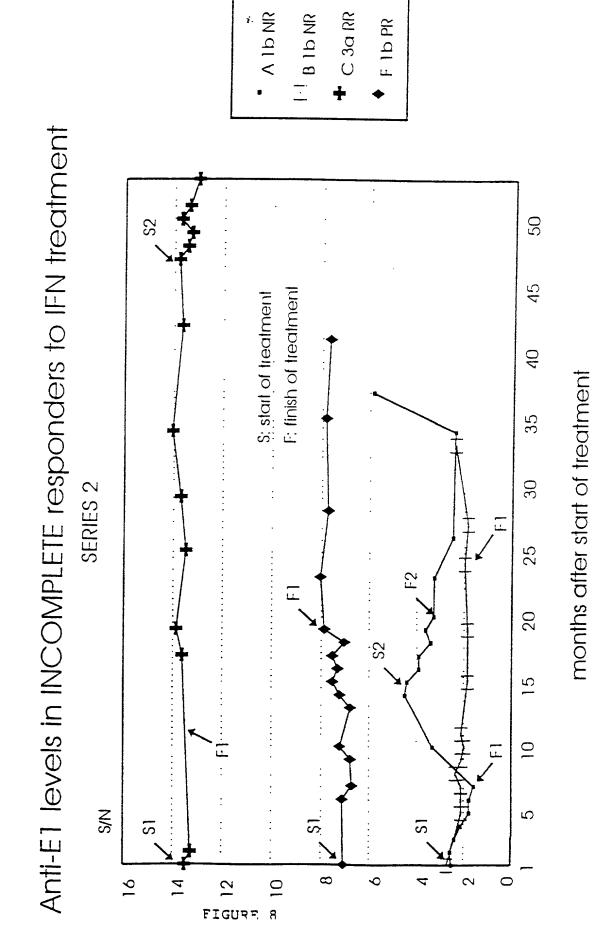
FIGURE 4

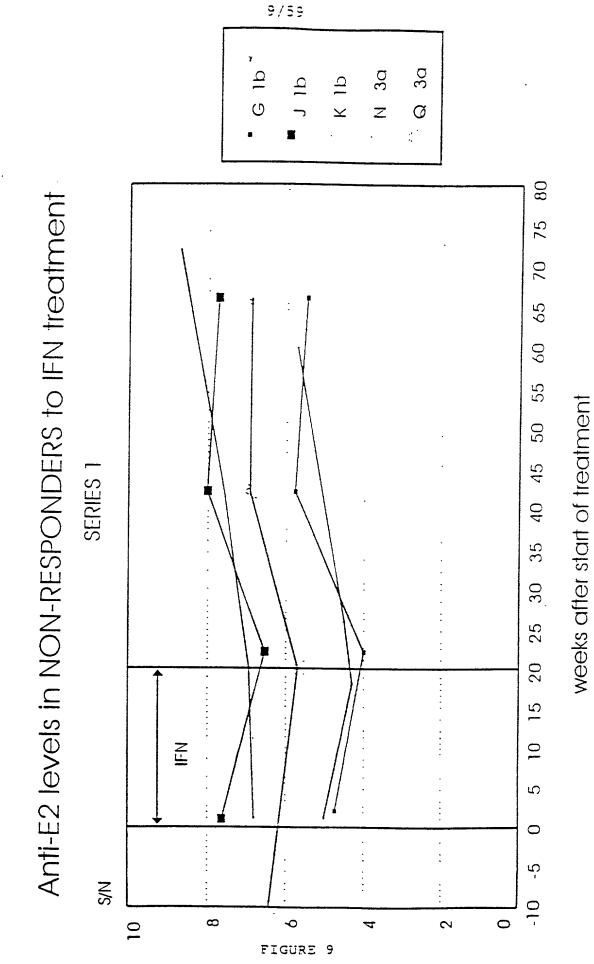


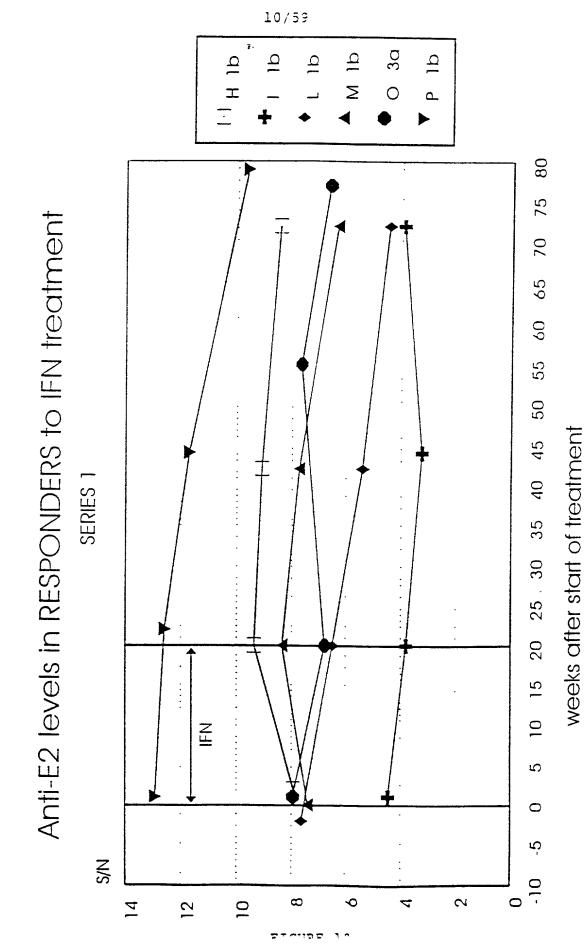
weeks after start of treatment

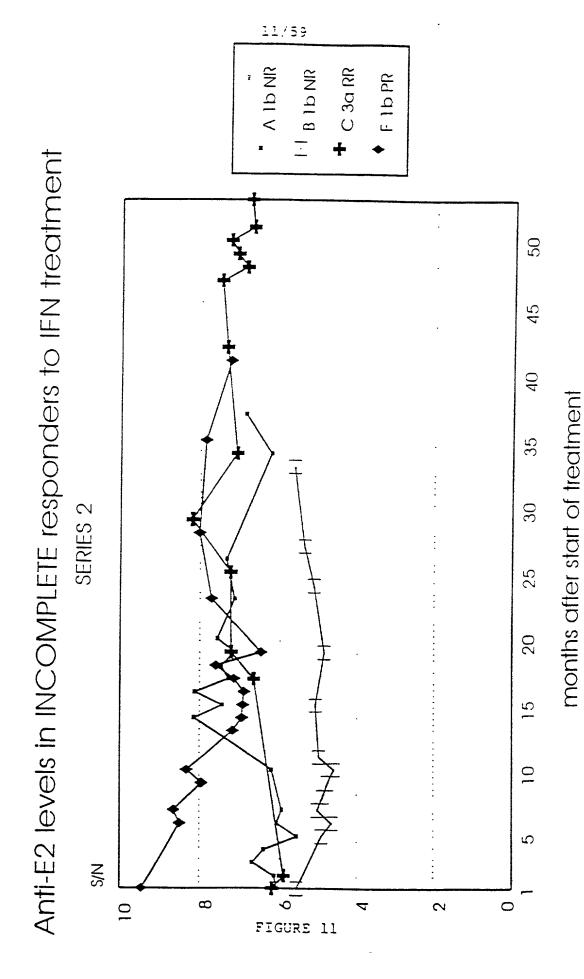
Σ 0 80 Anti-E1 levels in RESPONDERS to IFN treatment 70 9 weeks after start of treatment 50 40 SERIES 1 30 0 Z<u>H</u> 0 S/N  $\infty$ 9 2 0 12 2

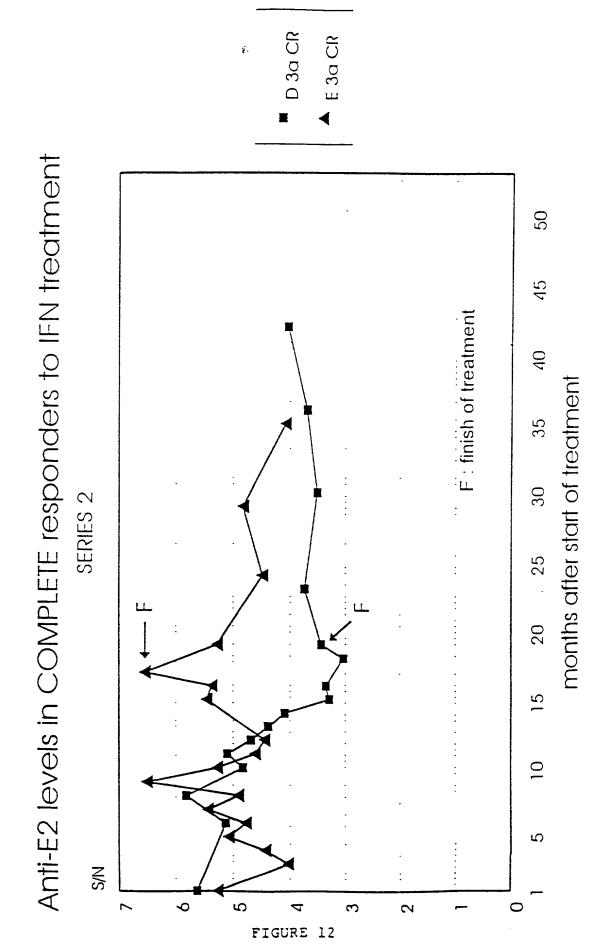
D 3a 3a ш Anti-E1 levels in patients with COMPLETE response to IFN 50 45 40 months after start of treatment 35 30 SERIES 2 25 20 15 10 2 S/N 9 10 2 0 FIGURE 7



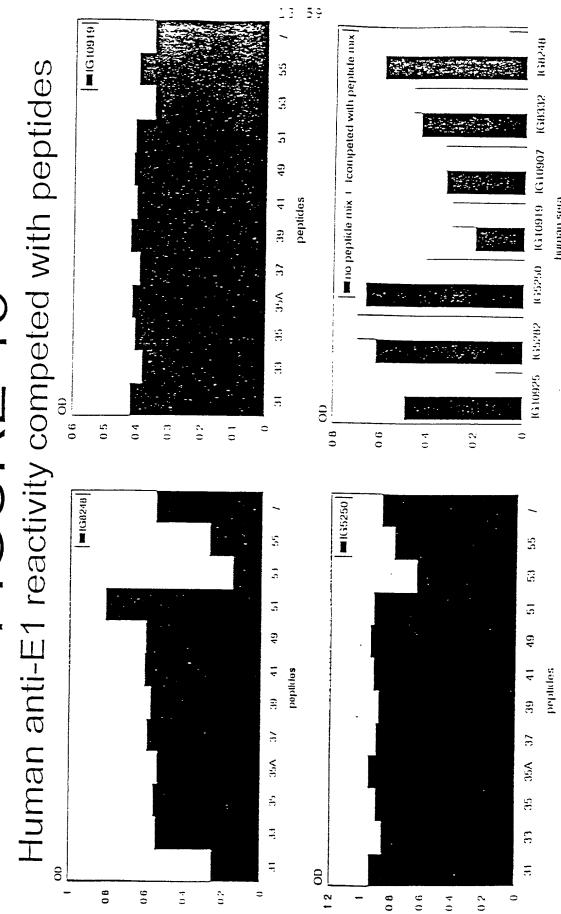






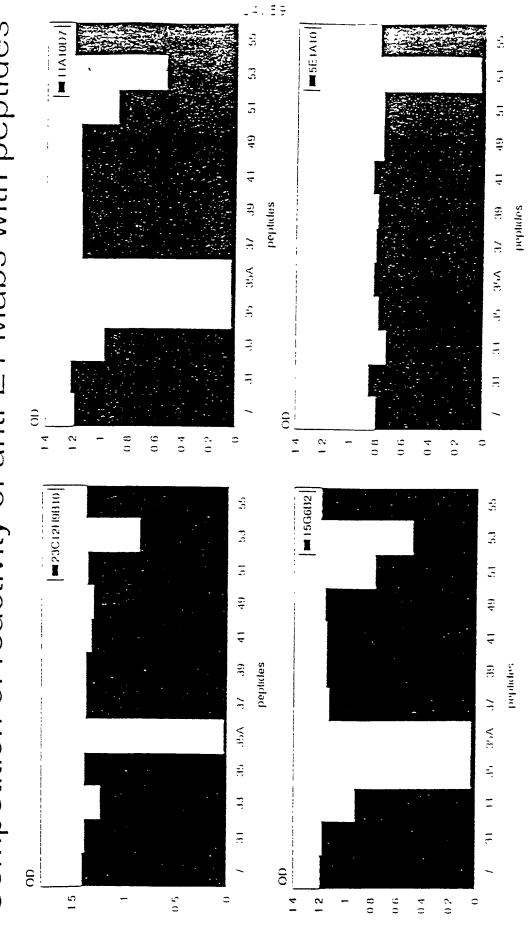


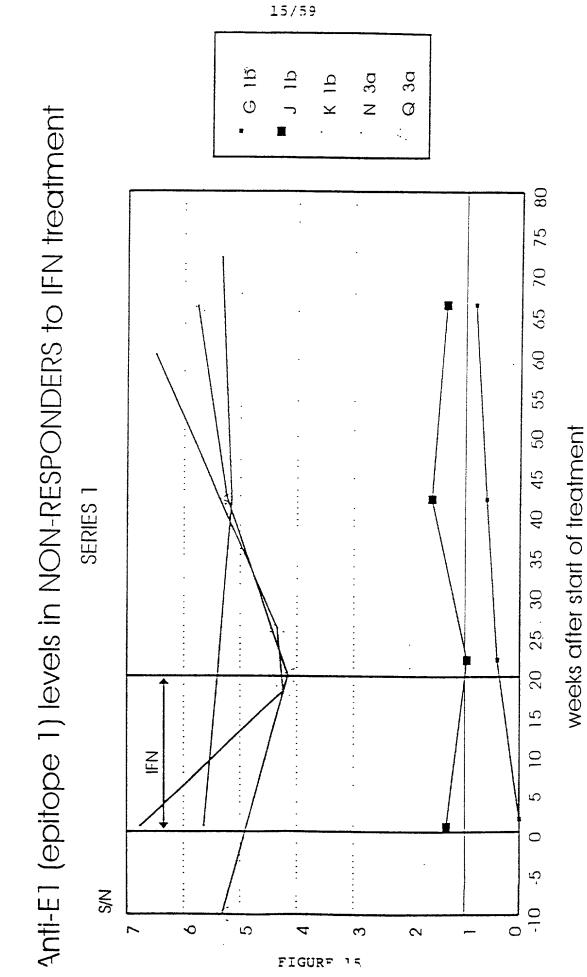
# FIGURE 13

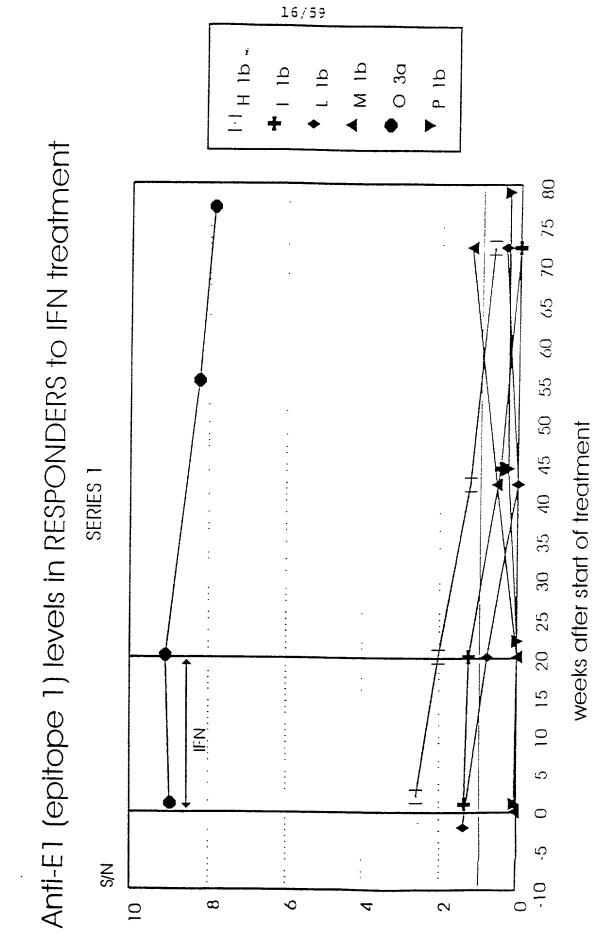


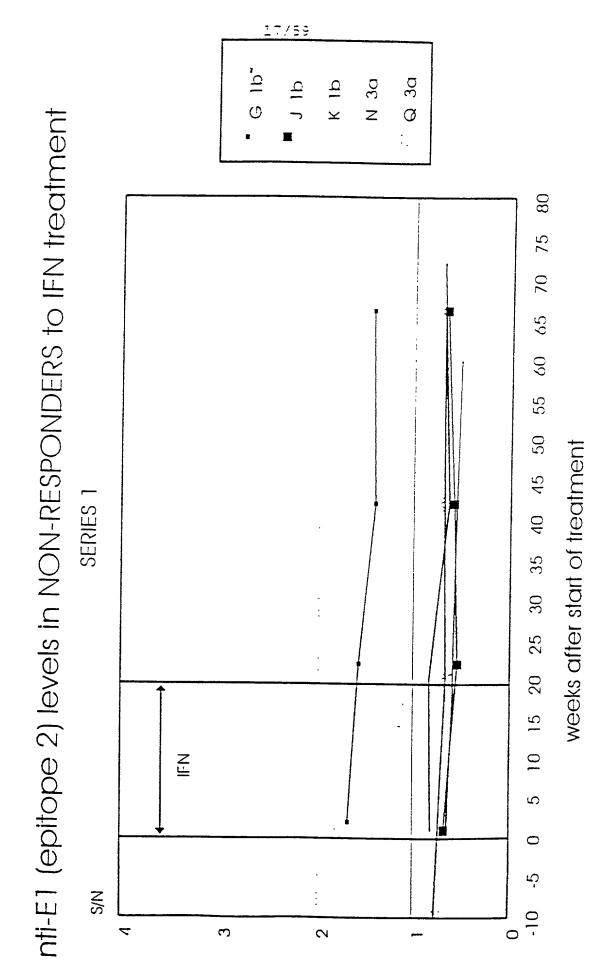
## FIGURE 14

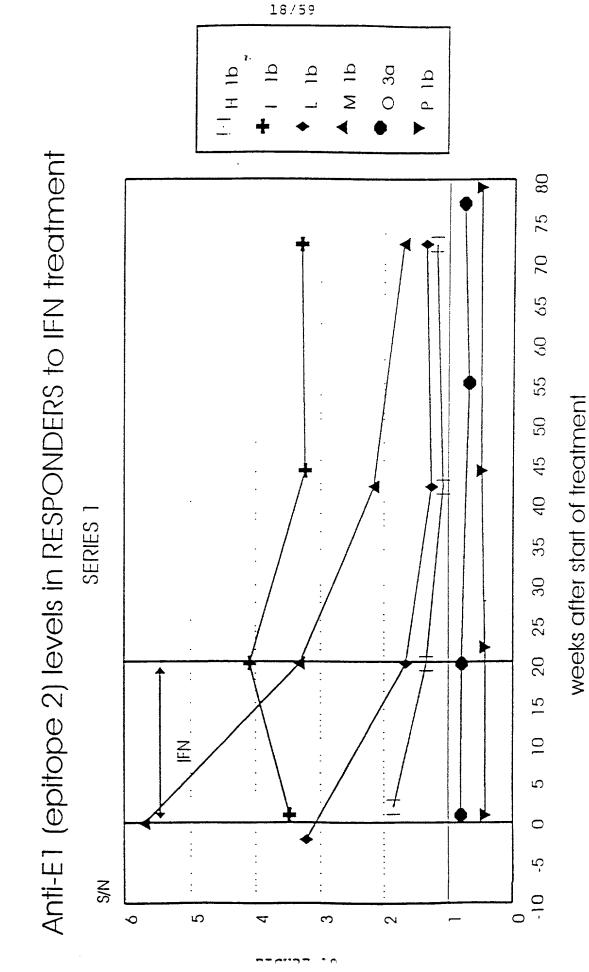
Competition of reactivity of anti-E1 Mabs with peptides

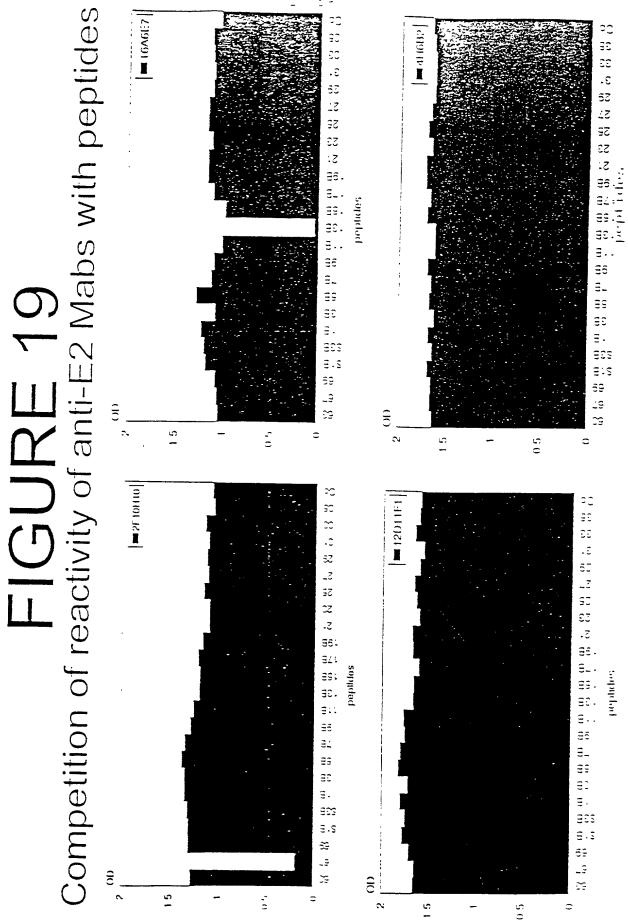




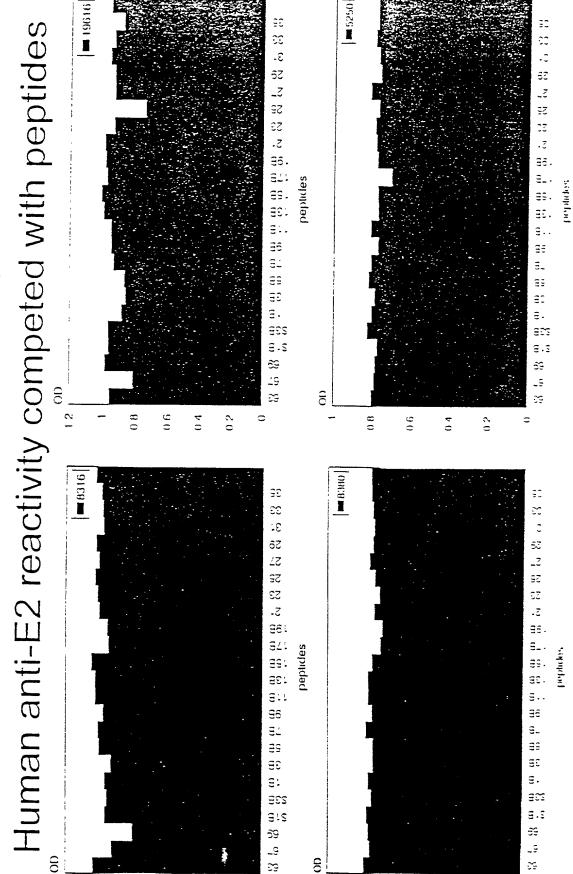








# FIGURE 20



### Figure 21

5' GGCATGCAAGCTTAATTAATTAATCGA5' (SEQ ID NO 1)
3'ACGTCCGTACGTTCGAATTAATTAATCGA5' (SEQ ID NO 94)

ř

5'CCGGGGAGGCCTGCACGTGATCGAGGGCAGCACCATCACCACCATCACTAATAGT
TAATTAACTGCA 3' (SEQ ID NO 2)

### SEC ID NO 3 (HCCI9A)

### SEQ ID NO 5 (HCCI10A)

### SEQ ID NO 7 (HCCI11A)

### SEQ ID NO 9 (HCCI12A)

### SEQ ID NO 11 (HCCI13A)

GCCCTGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTC
GCGGCCAGGAACGCCAGGCCACACGACAACGACAATACGACGCCACGTCGATTTGCTC
GTTGGGGCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCTTTT
CCTTGTTTCCCAGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCA
ACTGCTCAATCTATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAT
GAACTGGTAATAG

PCT/EP95/03031

### SEQ ID NO 13 (HCCI17A)

SEQ ID NO 15 (HCPr51)

ATGCCCGGTTGCTCTTTCTCTATCTT

SEQ ID NO 16 (HCPr52)
ATGTTGGGTAAGGTCATCGATACCCT

SEQ ID NO 17 (HCPr53)
CTATTAGGACCAGTTCATCATCATATCCCA

SEQ ID NO 18 (HCPr54)
CTATTACCAGTTCATCATCATATCCCA

SEQ ID NO 19 (HCPr107)

ATACGACGCCACGTCGATTCCCAGCTGTTCACCATC

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SEQ ID NO 20 (HCPr108)
GATGGTGAACAGCTGGGAATCGACGTGGCGTCGTAT

SEQ ID NO 21 (HCCI37)

### SEQ ID NO 23 (HCCI38)

SEQ ID NO 25 (HCC139)

ATGTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGCCTCCG
GGTTCTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT

ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCCCTGCGTTCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTCGATTCCCAGCTGTTCACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTTCGGGATCCTCTAATAG

### SEQ ID NO 27 (HCCI40)

### SEQ ID NO 29 (HCC162)

ATGGGTAAGGTCATCGATACCCTTACGTGCGGATCTCCATGGGGTACATCC
CGCTCGTCGGCGCTCCCGTAGGAGGCGTCGCAAGAGCCCTTGCGCATGGCGTGAGGGC
CCTTGAAGACGGGATAAATTTCGCAACAGGGAATTTGCCCGGTTGCTCCTTTTCTATTT
TCCTTCTCGCTCTGTTCTCTTGCTTAATTCATCCAGCAGCTAGTCTAGAGTGGCGGAAT
ACGTCTGGCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGTATTGTGTACGAGGC
CGATGACGTTATTCTGCACACACCCGGCTGCATACCTTGTGTCCAGGACGGCAATACA
TCCACGTGCTGGACCCCAGTGACACCTACAGTGGCAGTCAAGTACGTCGGAGCAACCA
CCGCTTCGATACGCAGTCATGTGGACCTATTAGTGGGCGCGGCCACGATGTGCTCTGC
GCTCTACGTGGGTGACATGTGTGGGGCTGTCTTCCTCGTGGGACAAGCCTTCACGTTCA
GACCTCGTCGCCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATCT
TTCAGGACATCGAATGGCTTGGGGATATGATGATGATGATGATAAG

WO 96/04385 PCT/EP95/03031 26/59

SEQ ID NO 31 (HCCI63)

ATGGGTAAGGTCATCGATACCCTAACGTGCGGATTCGCCGATCTCATGGGGTATATCC
CGCTCGTAGGCGGCCCCATTGGGGGGCCGCCAAGGGCTCTCGCACACGGTGTGAGGGT
CCTTGAGGACGGGGTAAACTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCT
TTATTCTTGCTCTTCTCTCGTGTCTGACCGTTCCGGCCTCTGCAGTTCCCTACCGAAATG
CCTCTGGGATTTATCATGTTACCAATGATTGCCCAAACTCTTCCATAGTCTATGAGGCA
GATAACCTGATCCTACACGGACCTGGTTGCGTGCCTTGTGTCATGACAGGTAATGTGA
GTAGATGCTGGGTCCAAATTACCCCTACACTGTCAGCCCCGAGCCTCGGAGCAGTCAC
GGCTCCTCTTCGGAGAGCCGTTGACTACCTAGCGGGAGGGGCTGCCCTCTGCTCCGCG
TTATACGTAGGAGACCGCTTGGGGACACTATTCTTGGTAGGCCAAATGTTCACCTATA
GGCCTCGCCAGCACGCTACGGTGCAGAACTGCAACTGTTCCATTTACAGTGGCCATGT
TACCGGCCACCGGATGGCATGGGATATGATGATGAACTGGTAATAG

SEQ ID NO 33 (HCPr109)
TGGGATATGATGATGAACTGGTC

SEQ ID NO 34 (HCPr72)
CTATTATGGTGGTAAKGCCARCARGAGCAGGAG

SEQ ID NO 35 (HCCL22A)

### SEQ ID NO 37 (HCCI41)

GATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCCATTGGGGAGTCCTGGCGG CCTCGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGGTTGATGCTACTCT TTGCCGGCGTCGACGGGCATACCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCA GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCGGCTCAGAAATCCAGCTCGTAAACAC AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAG CGCTTGGCCAGCTGTCGATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTT ACACTGAGCCTAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC GTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCC CGACTCGGATGTGCTGATTCTCAACACGCGGCGGCGCGCGGGGGCAACTGGTTCGGC TGTACATGGATGAATGGCACTGGGGTTCACCAAGACGTGTGGGGGCCCCCCGTGCAACA CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTT CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT TAGGATGTACGTGGGGGGGGGGGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCG AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG TCTACAACAGAGTGGCAGAGTGAGCTTAATTAATTAG

### SEQ ID NO 39 (HCCI42)

TTGCCGGCGTCGACGGGCATACCCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCA GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACAC AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAG CGCTTGGCCAGCTGTCGCTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTT ACACTGAGCCTAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC GTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCC CGACTCGGATGTGCTGATTCTCAACAACACGCGGCGCCGCGAGGCAACTGGTTCGGC TGTACATGGATGAATGGCACTGGGTTCACCAAGACGTGTGGGGGCCCCCCGTGCAACA CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTT CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCG AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG TCTACAACAGGTGATCGAGGGCAGACACCATCACCACCATCACTAATAG

### SEQ ID NO 41 (HCCI43)

ATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACG GGCATACCCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCT CTTTAGCCCCGGGTCGGCTCAGAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC ATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCAC TATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCG CTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGC TCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCG CGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGAC ATTCTCAACAACACGCGGCCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATG GCACTGGGTTCACCAAGACGTGTGGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCA ACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGC CAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGG CTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGG GGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGA CTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGTCTACAACAGAGTGG CAGAGCTTAATTAATTAG

WO 96/04385 PCT/EP95/03031

SEQ ID NO 43 (HCCI44)

ATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACG GGCATACCGGGTGTCAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCT CTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC ATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCAC TATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCG CTCCATCGACAAGTTCGCTGAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGC TCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCG CGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGAC ATTCTCAACAACACGCGGCCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATG GCACTGGGTTCACCAAGACGTGTGGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCA ACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCCGAGGCCACCTACGC CAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGG CTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGG GGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGA CTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGGTGAT CGAGGGCAGACACCATCACCACCATCACTAATAG

### SEQ ID NO 45 (HCCL64)

### SEQ ID NO 47 (HCCI65)

AATTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG GGTTCTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG CAACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTAT GAGGCAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGAGAAC AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG TCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGGCGGCTGCTTTCTG TTCCGCTATGTACGTGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCA CCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTCTATCCCGG CCACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTACAACG GCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGG GGGCCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACTGGGC TAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACGGGCATACCCGCGTGTCAG GAGGGGCAGCCTCCGATACCAGGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCGGC TCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAACAGGACTGCCCT GAACTGCAACGACTCCCCAAACAGGGTTCTTTGCCGCACTATTCTACAAACACAAA TTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCGCTCCATCGACAAGTTCG CTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGGCCCTA CTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGT CCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGGACGACCGATCGGTTTGGTGT CCCCACGTATAACTGGGGGGGGGAACGACTCGGATGTGCTGATTCTCAACACACGCGG CCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGGGTTCACCAAGA CGTGTGGGGGCCCCCCGTGCAACATCGGGGGGGGCCGGCAACACACCTTGACCTGCC

### SEQ ID NO 49 (HCCI66)

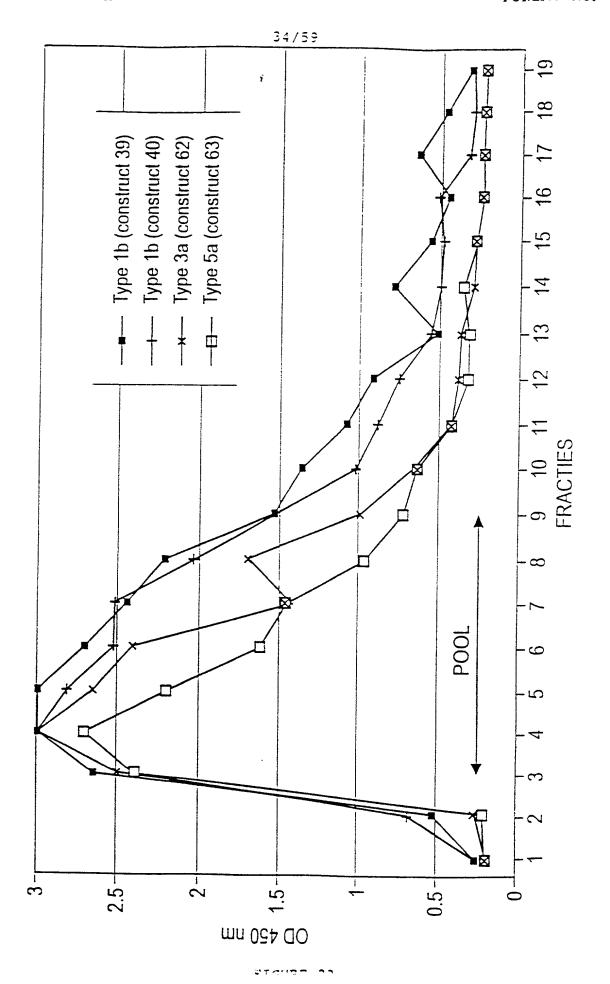
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TCGGCTCAGAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAACAGGACT GCCCTGAACTGCAACGACTCCCCAAACAGGGTTCTTTGCCGCACTATTCTACAAAC ACAAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCGCTCCATCGACAA GTTCGCTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGG CCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGT GCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGACGACCGATCGGTT TGGTGTCCCCACGTATAACTGGGGGGGCGAACGACTCGGATGTGCTGATTCTCAACAAC ACGCGGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGGGTTCA CCAAGACGTGTGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCAACACACCTTGA CCTGCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGCCAGATGCGGTTC TGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGGCTCTGGCACTAC CCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGGGGGGCGTGGAGC ACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGAGGACA GGGATAGATCAGAGCTTAGCCCGCTGCTGTCTACAACAGAGTGGCAGATACTGCC CTGTTCCTTCACCACCCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCAGAAC ATCGTGGACGTGCAATACCTGTACGGTGTAGGGTCGGCGGTTGTCTCCCTTGTCATCA AATGGGAGTATGTCCTGTTGCTCTTCCTCGGCAGACGCGCGCATCTGCGCCTGC TTATGGATGATGCTGATAGCTCAAGCTGAGGCCGCCTTAGAGAACCTGGTGGTCC TCAATGCGGCGGCCGTGGCCGGGGCGCATGGCACTCTTTCCTTGTGTTCTTCTGT GCTGCCTGGTACATCAAGGGCAGGCTGGTCCCTGGTGCGGCATACGCCTTCTATGGCG TGTGGCCGCTGCTCCTGCTGCCTGCCCTACCACCACGAGCTTATGCCTAGTAA

Figure 22

## OD measured at 450 nm construct

|                                          | Typ <del>:</del><br>Ib                                               | Type<br>Ib                                                                                                                                                                                | Тур:<br>Эа                       | 63<br>Type<br>5a                                                                                                                                                                          |
|------------------------------------------|----------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 | 0.981<br>0.812<br>0.373<br>0.633<br>0.441<br>0.321<br>0.525<br>0.351 | 1.954<br>0.085<br>0.051<br>0.550<br>2.603<br>2.967<br>2.810<br>2.499<br>2.481<br>1.970<br>1.422<br>0.926<br>0.781<br>0.650<br>0.432<br>0.371<br>0.348<br>0.374<br>0.186<br>0.171<br>0.164 | 0.151<br>0.098<br>0.099<br>0.083 | 1.142<br>0.120<br>0.050<br>0.057<br>2.372<br>2.694<br>2.154<br>1.561<br>1.390<br>0.865<br>0.604<br>0.519<br>0.294<br>0.199<br>0.209<br>0.184<br>0.151<br>0.106<br>0.108<br>0.090<br>0.087 |



## 35/59 Figure 24

|            |                |          |             | ured at 450 nm<br>nstruct |            |            |
|------------|----------------|----------|-------------|---------------------------|------------|------------|
| Fraction   | volume         | dilution | 39          | 40                        | 62         | 63         |
|            |                |          | Type<br>1b  | Type<br>1b                | Type<br>3a | Type<br>5a |
|            |                |          |             |                           |            |            |
| 20         | 250 <i>µ</i> l | 1/200    | 0 072       | 0.130                     | 0 096      | 0 051      |
| 21         | 200 μ.         | 1,200    | 0.109       | 0.193                     | 0.084      | 0.052      |
| 22         |                |          | 0.279       | 0.249                     | 0.00       | 0.052      |
| 23         |                | 0.093    | 0.151       | 0.297                     | 0 054      |            |
| 24         |                |          | 0.080       | 0 266                     | 0.438      | 0.056      |
| 25         |                |          | 0.251       | 0 100                     | 0 457      | 0.039      |
| 26         |                |          | 3           | 1 649                     | 0 722      | 0 066      |
| 27         |                |          |             | 3                         | 2 528      | 0 889      |
| 28         |                |          | 3<br>3<br>3 |                           | 3          | 2.345      |
| 29         |                |          | 3           | 3<br>3                    | 2 849      | 2.580      |
| 30         |                |          | 2.227       | 1 921                     | 1 424      | 1.333      |
| 31         |                |          | 0 263       | 0.415                     | 0.356      | 0.162      |
| 32         |                |          | 0.071       | 0.172                     | 0 154      | 0.064      |
| <b>3</b> 3 |                |          | 0.103       | 0 054                     | 0.096      | 0.057      |
| 34         |                |          | 0.045       | 0 045                     | 0 044      | 0 051      |
| 35         |                |          | 0 043       | 0.047                     | 0 045      | 0.046      |
| 36         |                |          | 0.045       | 0.045                     | 0 049      | 0.040      |
| 37         |                |          | 0 045       | 0.047                     | 0.046      | 0 048      |
| 38         |                |          | 0 046       | 0.048                     | 0.047      | 0 057      |
| 39         |                |          | 0 045       | 0.048                     | 0 050      | 0.057      |
| 40         |                |          | 0 046       | 0.049                     | 0 048      | 0 049      |

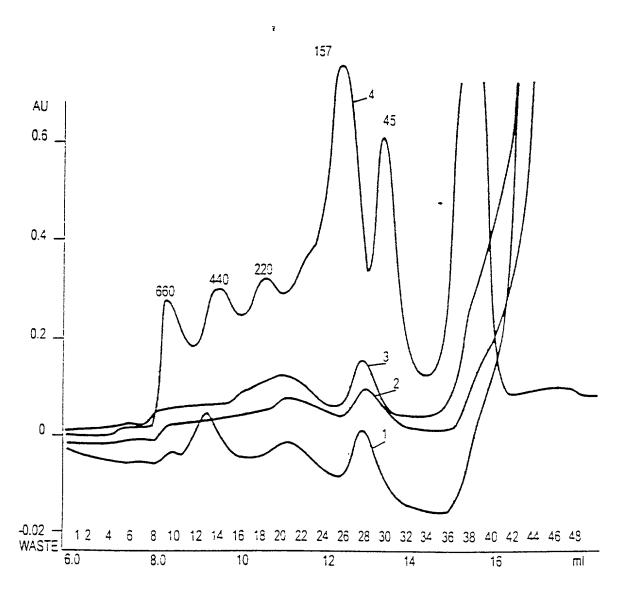


FIGURE 25

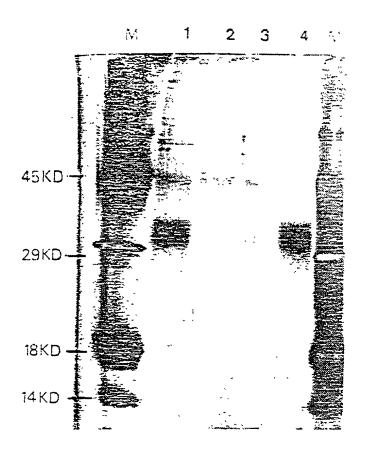


Figure 25

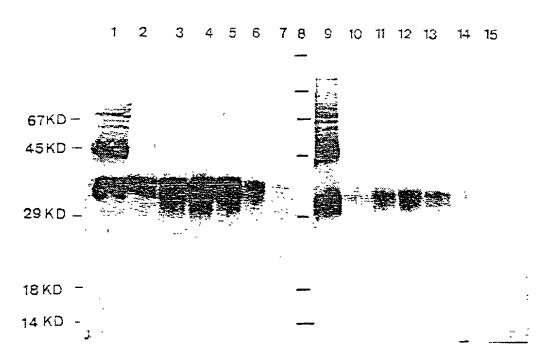


Figure 27

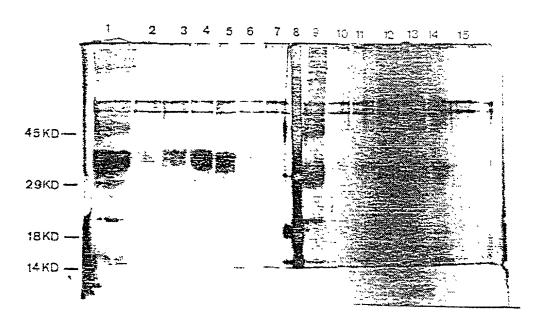
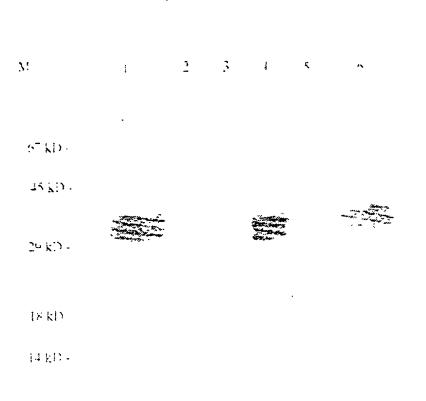


Figure 28

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Lane 1: Crude Lysate

Lane 2: Flow through Lentil Chromatography

Lanc 3: Wash with EMPIGEN Lentil Chromatography

Lanc 4: Eluate Lentil Chromatography

Lane 5: Flow through during concentration lental cluate

Lanc of Pool of Flatter Size Exclusion Chromatography

Figure 29: Western Blot Analysis with anti-E1 mouse monoclonal 5E1A10

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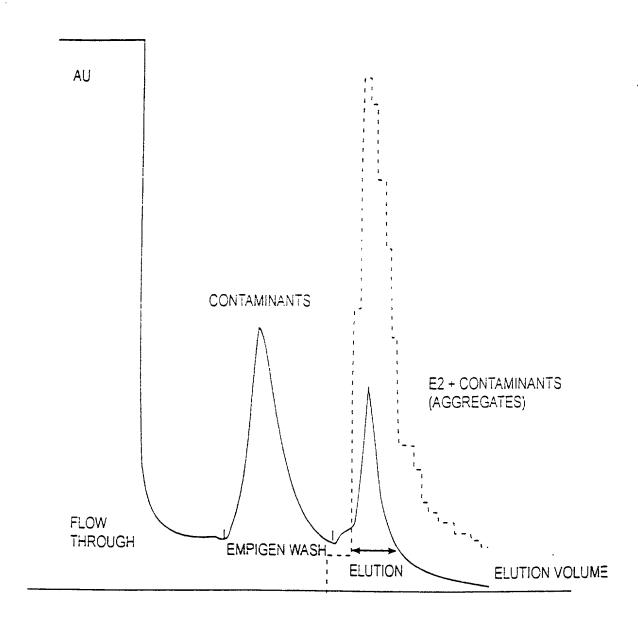
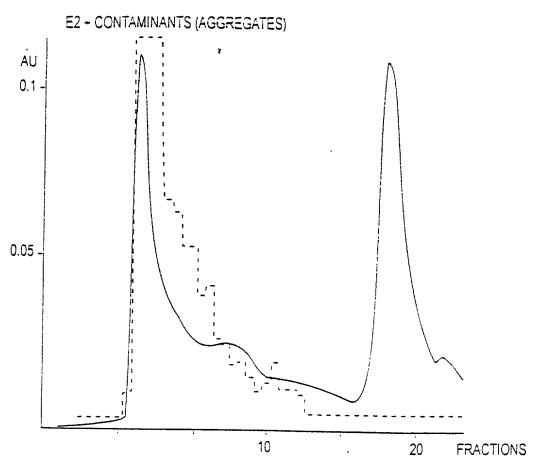


FIGURE 30

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#### A: NON - REDUCED



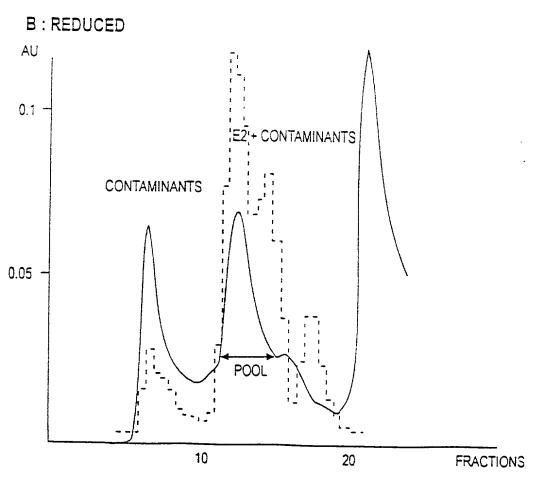


FIGURE 31

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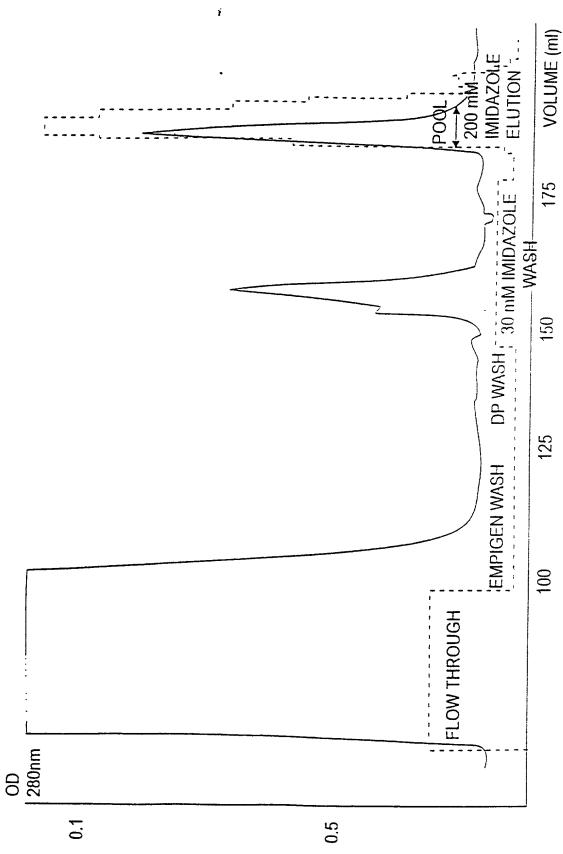
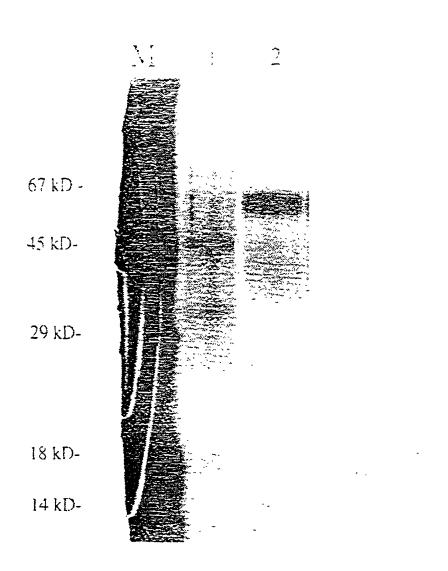


FIGURE 32

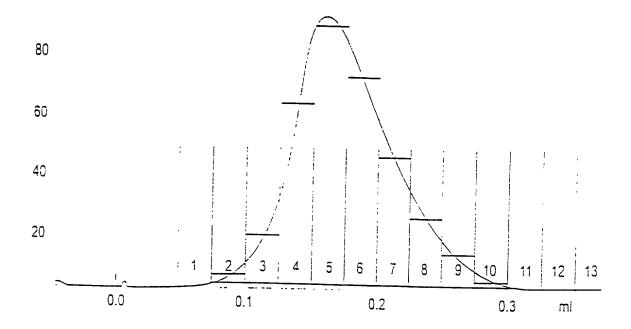
### FIGURE 33: SILVER STAIN OF PURIFIED E2



- 1. 30 mM: IMIDAZOLE WASH NI-IMAC
- 2. 0 f us E2

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45 59 Figure 34



| No. | Ret.<br>(ml) | Peak start<br>(ml) | Peak end (ml) | Dur<br>(ml) | Area<br>(ml≅mAU) | Height<br>(mAU) |
|-----|--------------|--------------------|---------------|-------------|------------------|-----------------|
| 1   | -0.45        | -0.46              | -0.43         | 0.04        | 0.0976           | 4.579           |
| 2   | 1.55         | 0.75               | 3.26          | 2.51        | 796.4167         | 889.377         |
| 3   | 3.27         | 3.26               | 3.31          | 0.05        | 0.0067           | 0.224           |
| 4   | 3.33         | 3.32               | 3.33          | 0.02        | 0.0002           | 0.018           |

Total number of detected peaks = 4

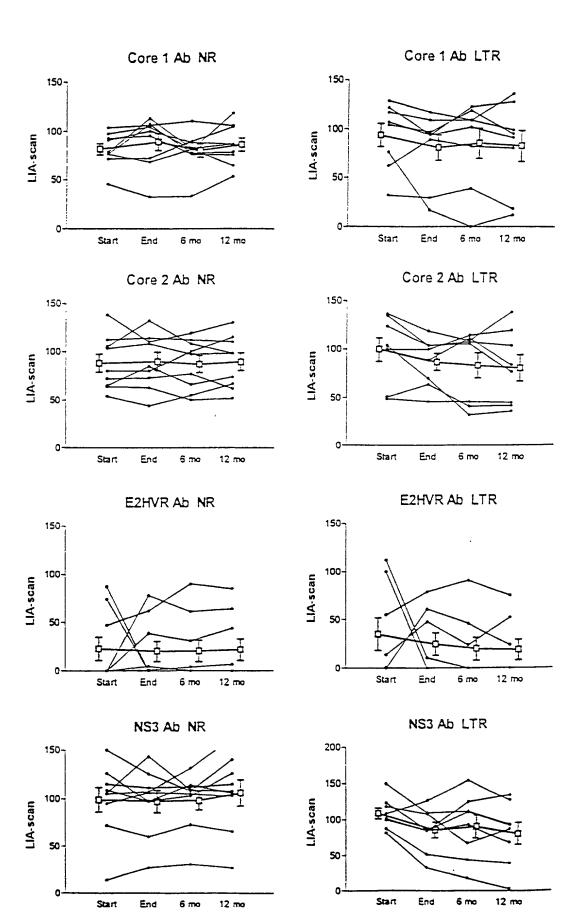
Total Area above baseline = 0.796522 ml\*AU

Total area in evaluated peaks = 0.796521 ml\*AU

Ratio peak area / total area = 0.999999

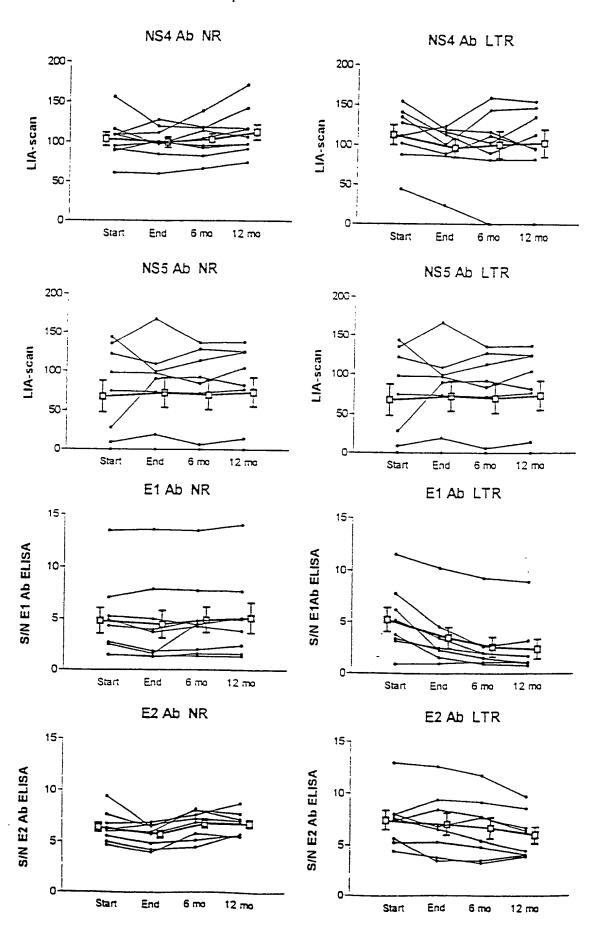
Total peak duration = 2.613583 ml

## FIGURE 35A



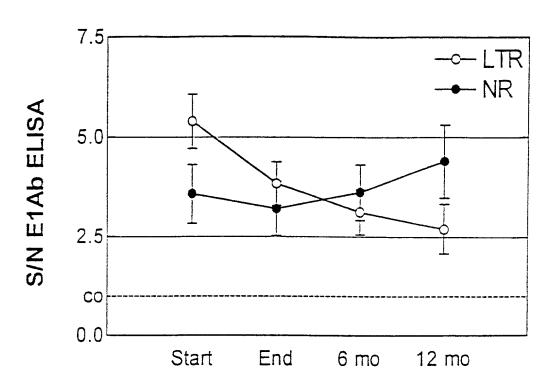
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## FIGURE 35B



Eigure 36

## E1 Ab



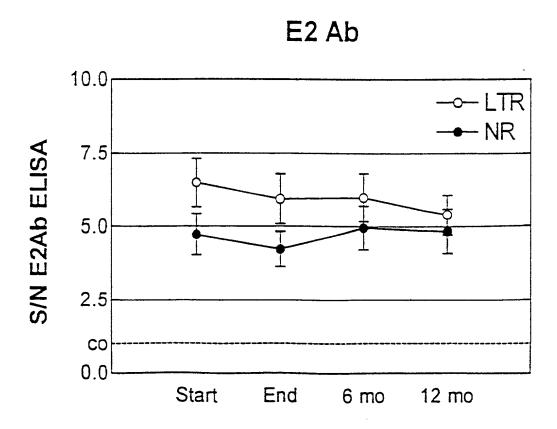
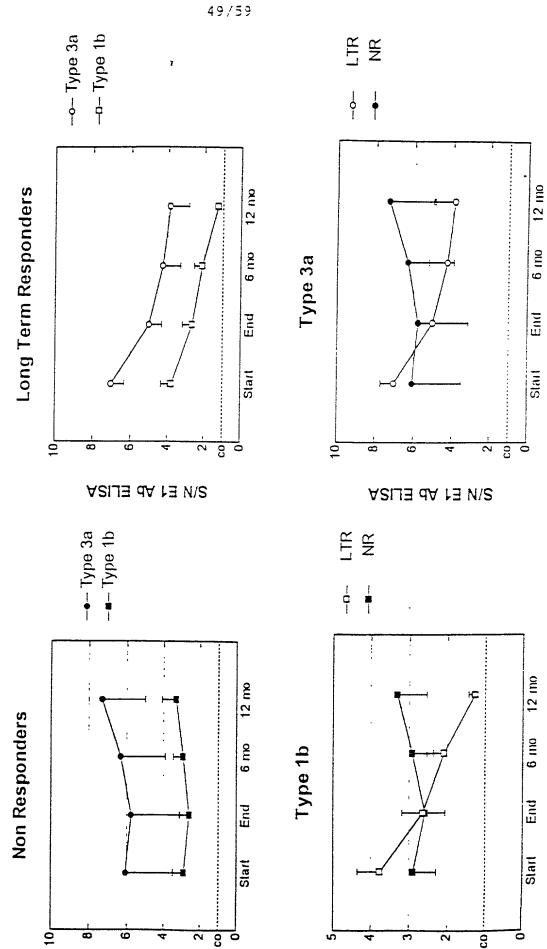
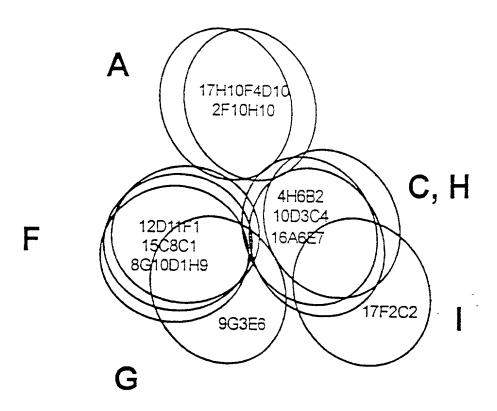


FIGURE 37



# Figure 38

# Relative Map Positions of anti-E2 monoclonal antibodies



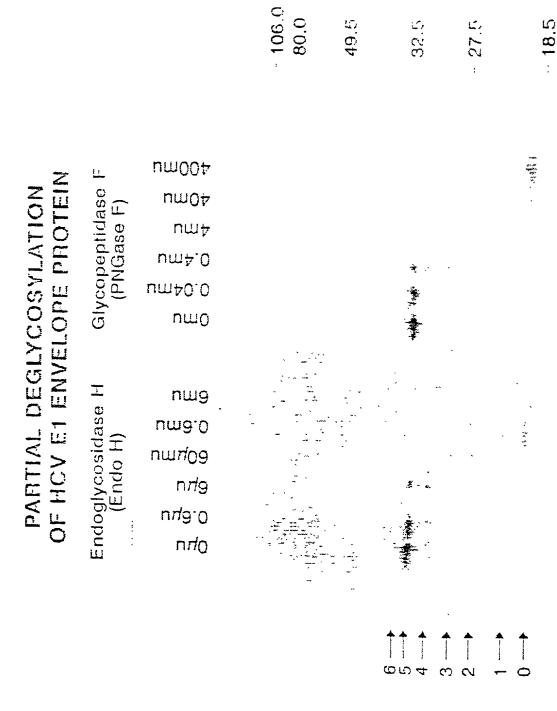


Figure 39

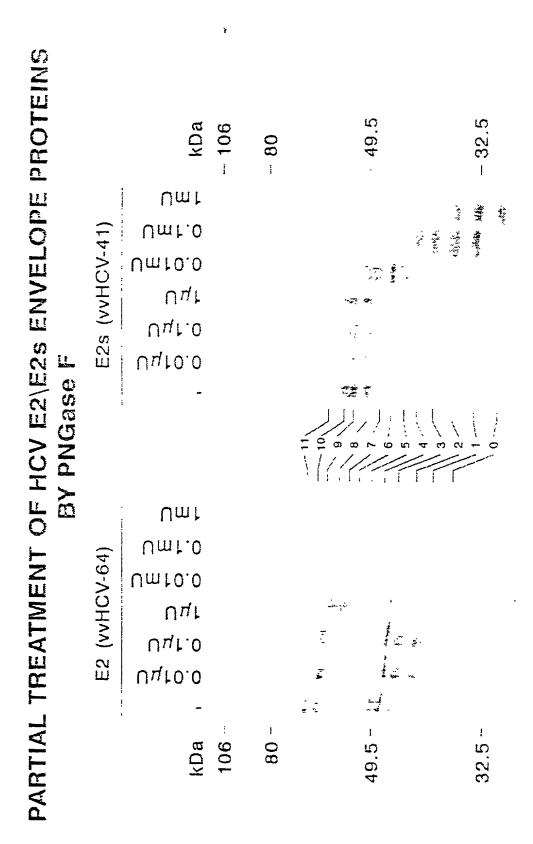
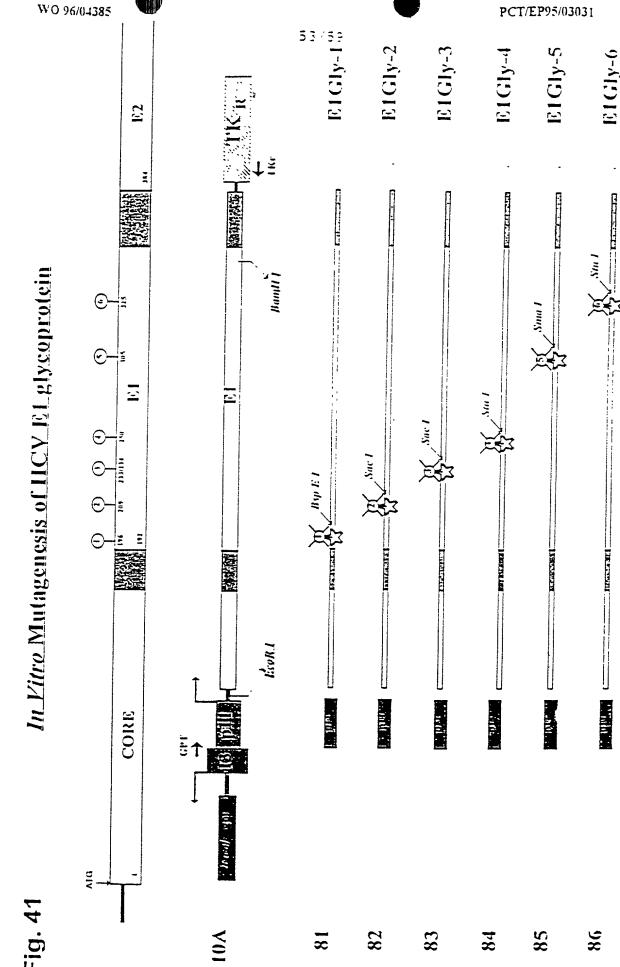
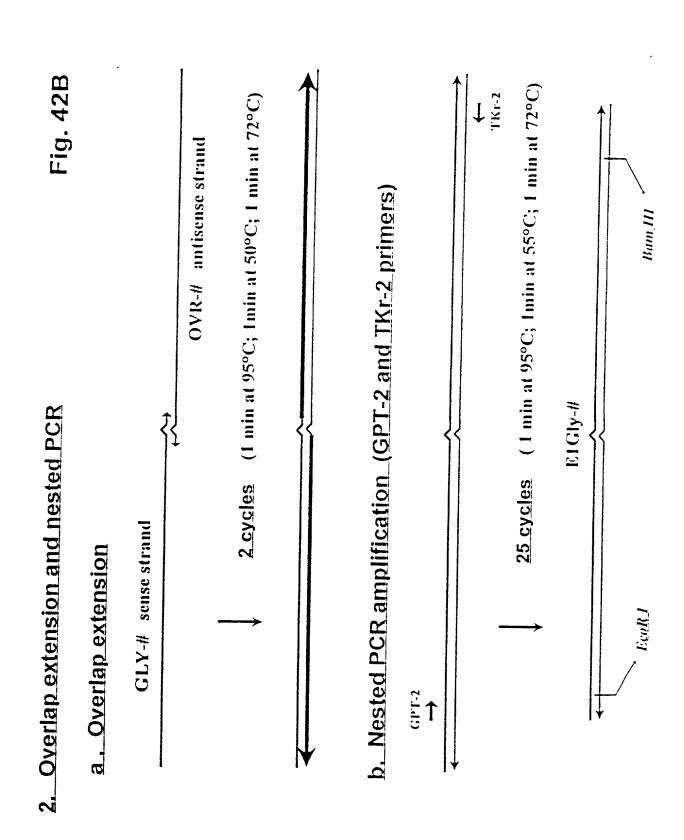


Figure 40



30 cycles (1 min at 95°C; 1 min at 50°C; 1 min at 72°C) In Vitro Mutagenesis of HCV E1 glycoprotein First step of PCR amplification (Gly-# and Ovr-# primers) BamILL 0VR-# ₹\$\$ **₹** 5 0vr-# GLY-# EcoR1 GPT CPT Fig. 42A



EIGly-2 EIGly-3 E1Gly-4 EIGly-1 EIGly-5 E2 ΥΞ In Vitro Mutagenesis of HCV E1 glycoprotein 9.H.O ⊕‡ Banell Bamll 1 6.30 n.t **⊙**-|¥ 770 nd 0.8.4 0718-3 ⊕-|₹ 770 111 Ecor. 1 CORE Fig. 43 82 83 84 85  $\frac{8}{2}$ 98

|      |                | HeLa cells                            |               | RK 13 cells |             |      |
|------|----------------|---------------------------------------|---------------|-------------|-------------|------|
|      |                | 2 4 6<br>1 3 5 7                      |               | 2 3 5 7     |             |      |
| 90.0 |                |                                       | — 80,0        |             |             | 80.0 |
| 49.5 | _              |                                       | <b>—</b> 49.5 |             | <del></del> | 49.5 |
| 32.5 | <del>-</del> . | * * * * * * * * * * * * * * * * * * * | 32.5          |             |             | 32.5 |
| 27.5 | ;              | •                                     | <b>— 27.5</b> |             |             | 27.5 |
| 18.5 |                |                                       | <b>—</b> 18.5 |             |             | 18.5 |

Figure 44A

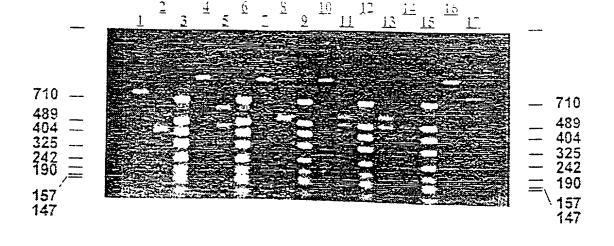


Figure 448





Figure 45

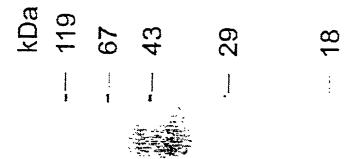


Figure 46